



#3

SEQUENCE LISTING

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<120> STABILIZED PROTEINS

<130> 9725-005-999

<140> 09/837,235

<141> 2001-04-18

<150> PCT/US00/28595

<151> 2000-10-16

<150> 60/159,763

<151> 1999-10-15

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<170> PatentIn version 3.0

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tcggcactca	ccaccgcact	ccgaaacgca	ggtgtctga	cccagatcg	gccaccacc	540
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<213> Candida antarctica

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					20				25			30			

Pro	Ile	Leu	Leu	Val	Pro	Gly	Thr	Gly	Thr	Thr	Gly	Pro	Gln	Ser	Phe
					35				40			45			

Asp	Ser	Asn	Trp	Ile	Pro	Leu	Ser	Thr	Gln	Leu	Gly	Tyr	Thr	Pro	Cys
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Trp	Ile	Ser	Pro	Pro	Pro	Phe	Met	Leu	Asn	Asp	Thr	Gln	Val	Asn	Thr
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 Asn Lys Leu Pro Val Leu Thr Trp Ser Gln Gly Gly Leu Val Ala Gln
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 Trp Gly Leu Thr Phe Phe Pro Ser Ile Arg Ser Lys Val Asp Arg Leu
 115 120 125
 Met Ala Phe Ala Pro Asp Tyr Lys Gly Thr Val Leu Ala Gly Pro Leu
 130 135 140
 Asp Ala Leu Ala Val Ser Ala Pro Ser Val Trp Gln Gln Thr Thr Gly
 145 150 155 160
 Ser Ala Leu Thr Thr Ala Leu Arg Asn Ala Gly Gly Leu Thr Gln Ile
 165 170 175
 Val Pro Thr Thr Asn Leu Tyr Ser Ala Thr Asp Glu Ile Val Gln Pro
 180 185 190
 Gln Val Ser Asn Ser Pro Leu Asp Ser Ser Tyr Leu Phe Asn Gly Lys
 195 200 205
 Asn Val Gln Ala Gln Ala Val Cys Gly Pro Leu Phe Val Ile Asp His
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 Ala Gly Ser Leu Thr Ser Gln Phe Ser Tyr Val Val Gly Arg Ser Ala
 225 230 235 240
 Leu Arg Ser Thr Thr Gly Gln Ala Arg Ser Ala Asp Tyr Gly Ile Thr
 245 250 255
 Asp Cys Asn Pro Leu Pro Ala Asn Asp Leu Thr Pro Glu Gln Lys Val
 260 265 270
 Ala Ala Ala Ala Leu Leu Ala Pro Ala Ala Ala Ile Val Ala Gly
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aaggttcaaa agcaatttaa gtatgttaac gcggccgcag caacattgga tgaaaaagct    180
gtaaaagaat tgaaaaaaga tccgagcggtt gcatatgtgg aagaagatca tattgcacat   240
gaatatgcgc aatctgttcc ttatggcatt tctcaaatta aagcgccggc tcttcactct   300
caaggctaca caggctctaa cgtaaaagta gctgttatcg acagcggaat tgactcttct   360
catcctgact taaacgtcag aggcggagca agcttcgtac cttctgaaac aaaccctatac   420
caggacggca gttctcacgg tacgcatgta gccggtaga ttgcgcgtct taataactca    480
atcggtgttc tggcgtag cccaaagcgca tcattatatg cagtaaaagt gcttgattca   540
acaggaagcg gccaatatacg ctggattatt aacggcattg agtgggcccatt ttccaacaat  600
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gcggtaa	aca	gcagcaacca	aagagcttca	ttctccagcg	cagg	ttctga	840	
atggctc	c	ctg	tcgttccat	ccaaagcaca	cttc	ctggag	900	
gaa	acgtcca	tggcactcc	tcacgttgc	ggagcagcag	cgtt	aaattct	960	
ccgactt	gga	caaacgcgca	agtccgtgat	cgtttagaaa	gcact	gcaac	1020	
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		20				25						30			
Asp	Val	Ile	Ser	Glu	Lys	Gly	Gly	Lys	Val	Gln	Lys	Gln	Phe	Lys	Tyr
		35				40					45				
Val	Asn	Ala	Ala	Ala	Ala	Thr	Leu	Asp	Glu	Lys	Ala	Val	Lys	Glu	Leu
		50				55				60					
Lys	Lys	Asp	Pro	Ser	Val	Ala	Tyr	Val	Glu	Glu	Asp	His	Ile	Ala	His
		65			70				75			80			
Glu	Tyr	Ala	Gln	Ser	Val	Pro	Tyr	Gly	Ile	Ser	Gln	Ile	Lys	Ala	Pro
		85				90						95			
Ala	Leu	His	Ser	Gln	Gly	Tyr	Thr	Gly	Ser	Asn	Val	Lys	Val	Ala	Val
		100				105					110				
Ile	Asp	Ser	Gly	Ile	Asp	Ser	Ser	His	Pro	Asp	Leu	Asn	Val	Arg	Gly
		115			120						125				
Gly	Ala	Ser	Phe	Val	Pro	Ser	Glu	Thr	Asn	Pro	Tyr	Gln	Asp	Gly	Ser
		130			135						140				
Ser	His	Gly	Thr	His	Val	Ala	Gly	Thr	Ile	Ala	Ala	Leu	Asn	Asn	Ser
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Ile Glu Trp Ala Ile Ser Asn Asn Met Asp Val Ile Asn Met Ser Leu		
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Gly Gly Pro Thr Gly Ser Thr Ala Leu Lys Thr Val Val Asp Lys Ala		
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Val Ser Ser Gly Ile Val Val Ala Ala Ala Gly Asn Glu Gly Ser		
225	230	235
Ser Gly Ser Thr Ser Thr Val Gly Tyr Pro Ala Lys Tyr Pro Ser Thr		
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Ile Ala Val Gly Ala Val Asn Ser Ser Asn Gln Arg Ala Ser Phe Ser		
260	265	270
Ser Ala Gly Ser Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln		
275	280	285
Ser Thr Leu Pro Gly Gly Thr Tyr Gly Ala Tyr Asn Gly Thr Ser Met		
290	295	300
Ala Thr Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His		
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Pro Thr Trp Thr Asn Ala Gln Val Arg Asp Arg Leu Glu Ser Thr Ala		
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Thr Tyr Leu Gly Asn Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val		
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Gln Ala Ala Ala Gln		
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Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser		
35	40	45

Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr
 50 55 60

His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu
 65 70 75 80

Gly Val Ala Pro Asn Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala
 85 90 95

Ser Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
 100 105 110

Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
 115 120 125

Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly
 130 135 140

Val Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser
 145 150 155 160

Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln
 165 170 175

Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile
 180 185 190

Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr
 195 200 205

Ala Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala
 210 215 220

Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile
 225 230 235 240

Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
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Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
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20

25

30

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 35 40 45

Ser Phe Val Pro Ser Glu Thr Asn Pro Tyr Gln Asp Gly Ser Ser His
 50 55 60

Gly Thr His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly
 65 70 75 80

Val Leu Gly Val Ser Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
 85 90 95

Asp Ser Thr Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
 100 105 110

Trp Ala Ile Ser Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
 115 120 125

Pro Thr Gly Ser Thr Ala Leu Lys Thr Val Val Asp Lys Ala Val Ser
 130 135 140

Ser Gly Ile Val Val Ala Ala Ala Gly Asn Glu Gly Ser Ser Gly
 145 150 155 160

Ser Thr Ser Thr Val Gly Tyr Pro Ala Lys Tyr Pro Ser Thr Ile Ala
 165 170 175

Val Gly Ala Val Asn Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Ala
 180 185 190

Gly Ser Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
 195 200 205

Leu Pro Gly Gly Thr Tyr Gly Ala Tyr Asn Gly Thr Cys Met Ala Thr
 210 215 220

Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Thr
 225 230 235 240

Trp Thr Asn Ala Gln Val Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr
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35 40 45

Ser Phe Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His
50 55 60

Gly Thr His Val Ala Gly Thr Val Leu Ala Val Ala Pro Ser Ala Ser
65 70 75 80

Leu Tyr Ala Val Lys Val Leu Gly Ala Asp Gly Ser Gly Gln Tyr Ser
85 90 95

Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn Asn Met Asp Val
100 105 110

Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Ala Ala Leu Lys Ala
115 120 125

Ala Val Asp Lys Ala Val Ala Ser Gly Val Val Val Val Ala Ala Ala
130 135 140

Gly Asn Glu Gly Thr Ser Gly Ser Ser Ser Thr Val Gly Tyr Pro Gly
145 150 155 160

Lys Tyr Pro Ser Val Ile Ala Val Gly Ala Val Asp Ser Ser Asn Gln
165 170 175

Arg Ala Ser Phe Ser Ser Val Gly Pro Glu Leu Asp Val Met Ala Pro
180 185 190

Gly Val Ser Ile Cys Ser Thr Leu Pro Gly Asn Lys Tyr Gly Ala Lys
195 200 205

Ser Gly Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Ala Ala Leu
210 215 220

Ile Leu Ser Lys His Pro Asn Trp Thr Asn Thr Gln Val Arg Ser Ser
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